SEQUENCE LISTING

<110> Oy Jurilab Ltd

<120> Method for detecting the risk of acute myocardial infarction and coronary heart disease

<130> 40597

<160> 56

<170> PatentIn version 3.1

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Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
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gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac 144
Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
35 40 45

ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc 192
Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50 55 60

atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc 240
Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65 70 75 80

cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc 288
Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
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acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg 336
Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
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gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc 384
Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
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                165                 170                 175

agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac      576
Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
            180                 185                 190

ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg      624
Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
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gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac      672
Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
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His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
225                 230                 235                 240

gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag      768
Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
                245                 250                 255

gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc      816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
            260                 265                 270

agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt      864
Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
        275                 280                 285

tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag      912
Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
    290                 295                 300

gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc      960
Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
305                 310                 315                 320

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Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
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Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
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Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
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gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc     1152
Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
    370                 375                 380

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405 410 415

tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt 1296
Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
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Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
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Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
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Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
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Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
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Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
        195                 200                 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
    210                 215                 220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
225                 230                 235                 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
                245                 250                 255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
            260                 265                 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
        275                 280                 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
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Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
305                 310                 315                 320

Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
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Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
            340                 345                 350

Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
        355                 360                 365

Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
    370                 375                 380

Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
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Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
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Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
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gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg       96
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gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac      144

Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
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ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc      192
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atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc      240
Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
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cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc      288
Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
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acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg      336
Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
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gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc      384
Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
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atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg      432
Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
    130                 135                 140

ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg      480
Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
145                 150                 155                 160
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cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc      528

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
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agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac      576
Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
            180                 185                 190

ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg      624
Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
        195                 200                 205

gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac      672
Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
    210                 215                 220

cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg      720
His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
225                 230                 235                 240

gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag      768
Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
                245                 250                 255

gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc      816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
            260                 265                 270

agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt      864
Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
        275                 280                 285

tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag      912

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
    290                 295                 300

gag gag gag gaa gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc      960
Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
305                 310                 315                 320

tca gct tgc agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg     1008
Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu
                325                 330                 335

gcc acc cta cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata     1056
Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
            340                 345                 350

ggt ggg cag tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc     1104
Gly Gly Gln Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg
        355                 360                 365

ttc acc ttc gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg     1152
Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
    370                 375                 380

ttc ccc ttc ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac     1200
Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His
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tgc aac agc tca ctg aac cct gtt atc tac acc atc ttc aac cag gac     1296

Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
            420                 425                 430

ttc cgc cgt gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg     1344
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Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
        35                  40                  45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
    50                  55                  60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
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Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
                85                  90                  95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
            100                 105                 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
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Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
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Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
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Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
                165                 170                 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
            180                 185                 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
        195                 200                 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
    210                 215                 220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
225                 230                 235                 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
                245                 250                 255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
            260                 265                 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
        275                 280                 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
    290                 295                 300

Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
305                 310                 315                 320

Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu
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Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
            340                 345                 350

Gly Gly Gln Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg
        355                 360                 365

Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
    370                 375                 380

Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His
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Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
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Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
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tgactaacac atagctagta agatttcttg tcacttacga caaagacatg aattttctcc 180

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aaccaaagca gtgcaagatt cagttcaagg tcctgaaaaa agaaaaacat tttactctgt 480

gtaccttgtg tctttctaaa tttctctctc caaagtaaag ttcaagcatt aaacttagtg 540

tgtttgacct ttttaatttt cttttctttt tccttttttt tcttttgctt tgttatatgg 600

tggtttgtat ggttccttt 619

<210> 28
<211> 619
<212> DNA
<213> Homo sapiens
<400> 28
ggatgaagca gaatgaagag taggtaaccc tgaggttgag aggtatattg ttggaccagg 60

gagcaggtaa taaatacatc ctggatagac tcacatgggg aaaaaaacta tgatcttgca 120

tgactaacac atagctagta agatttcttg tcacttacga caaagacatg aattttctcc 180

atcctaacat gactgataca gtgtctctta tttagactat ctcagttagt ctggctgtgc 240

ttgtcctttt tcccacctcc ctcgctgtgc ctgaccctct cttctttcca caggttctca 300

ggcaagagcc acctgctatt gccgaaccgg ccgttgtgct acccgtgagt ccctctccgg 360

ggtgtgtgaa atcagtggcc gcctctacag actctgctgt cgctgagctt cctagataga 420

aaccaaagca gtgcaagatt cagttcaagg tcctgaaaaa agaaaaacat tttactctgt 480

gtaccttgtg tctttctaaa tttctctctc caaaataaag ttcaagcatt aaacttagtg 540

tgtttgacct ttttaatttt cttttctttt tccctttttt tcttttgctt tgttatatgg 600

tggtttgtat ggttccttt 619

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 29
ggatgaagca gaatgaaga 19

<210> 30
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 30

aaaggaacca tacaaacca 19

<210> 31
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Sequencing primer
<400> 31
gttagtctgg ctgtgctt 18

<210> 32
<211> 1052
<212> DNA
<213> Homo sapiens
<400> 32
gggctactga gtttggtgaa aagataagac tcctgaaaat tctattgatt ctcttttgaa 60

cttctttctt aaattagttt tatgatggac ttggctctca ttggtatttc ccaagattat 120

ggagatggga tagtgatgtc tgacaagtac ctaagatgct aagttgaagg tctaaaattc 180

catcctaaaa gcaaataatt actctatcat ctacgtgccc tttgcttctt aaagttactc 240

aaggaaggca gactaaacag gaaatttact ttggattcaa gaggggcata gagacgctct 300

cagcctgccc atttgccttc atcaacattc ctaaacactg ggcttaaaat gtagtatgag 360

taaactctct cttagtctat ccatctccca ctagcagttt taacatcatc tctagttatt 420

aaccttggct caatggcttt ctcctctttt tttatacaga atttattggc ttgagacgct 480

gtttaatggg tttggggaga tgcagggatc actgcaatgt ggatgaaaaa gagatacaga 540

aatgcaagat gaaaaaatgt tgtgttggac caaaagtggt taaattgatt aaaaactacc 600

tgcaatatgg aacaccaaat gtacttaatg aagacgtcca agaaatgcta aaacctgcca 660

agaattctag tgctgtgata caaagaaaac atattttatc tgttctcccc caaatcaaaa 720

gcactagctt ttttgctaat accaactttg tcatcattcc aaatgccacc cctatgaact 780

ctgccaccat cagcactatg accccaggac agatcacata cactgctact tctaccaaga 840

gtaacaccaa agaaagcaga gattctgcca ctgcctcgcc accaccagca ccacctccac 900

caaacatact gccaacacca tcactggagc tagaggaagc agaagagcag taatgtggat 960

ctttccctta aaactccaag ttcctctcta tttttgctat ctataaaatg acatagaact 1020

gtttcctctg tcatcagtca ttcaataaac ac 1052

<210> 33
<211> 1049
<212> DNA
<213> Homo sapiens
<400> 33

gggctactga gtttggtgaa aagataagac tcctgaaaat tctattgatt ctcttttgaa 60

cttctttctt aaattagttt tatgatggac ttggctctca ttggtatttc ccaagattat 120

ggagatggga tagtgatgtc tgacaagtac ctaagatgct aagttgaagg tctaaaattc 180

catcctaaaa gcaaataatt actctatcat ctacgtgccc tttgcttctt aaagttactc 240

aaggaaggca gactaaacag gaaatttact ttggattcaa gaggggcata gagacgctct 300

cagcctgccc atttgccttc atcaacattc ctaaacactg ggcttaaaat gtagtatgag 360

taaactctct cttagtctat ccatctccca ctagcagttt taacatcatc tctagttatt 420

aaccttggct caatggcttt ctctttttt atacagaatt tattggcttg agacgctgtt 480

taatgggttt ggggagatgc agggatcact gcaatgtgga tgaaaaagag atacagaaat 540

gcaagatgaa aaaatgttgt gttggaccaa aagtggttaa attgattaaa aactacctgc 600

aatatggaac accaaatgta cttaatgaag acgtccaaga aatgctaaaa cctgccaaga 660

attctagtgc tgtgatacaa agaaaacata ttttatctgt tctcccccaa atcaaaagca 720

ctagcttttt tgctaatacc aactttgtca tcattccaaa tgccacccct atgaactctg 780

ccaccatcag cactatgacc ccaggacaga tcacatacac tgctacttct accaagagta 840

acaccaaaga aagcagagat tctgccactg cctcgccacc accagcacca cctccaccaa 900

acatactgcc aacaccatca ctggagctag aggaagcaga agagcagtaa tgtggatctt 960

tcccttaaaa ctccaagttc ctctctattt ttgctatcta taaaatgaca tagaactgtt 1020

tcctctgtca tcagtcattc aataaacac 1049

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 34
ggctactgag tttggtga 18

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 35
gtgtttattg aatgactgat g 21

<210> 36
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequencing primer
<400> 36
caaggaaggc agactaaa 18

<210> 37
<211> 552
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1)..(552)
<223> Coding sequence for the variant human DEFB129 gene
<400> 37

```
atg aag ctc ctt ttt cct atc ttt gcc agc ctc atg cta cag tac cag      48
Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
1               5                   10                  15

gtg aac aca gaa ttt att ggc ttg aga cgc tgt tta atg ggt ttg ggg      96
Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
            20                  25                  30

aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc     144
Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
        35                  40                  45

aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa     192
Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
    50                  55                  60

aac tac ctg caa tat gga aca cca aat gta ctt aat gaa gac gtc caa     240
Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
65                  70                  75                  80

gaa atg cta aaa cct gcc aag aat tct agt gct gtg ata caa aga aaa     288
Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
                85                  90                  95

cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct     336
His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
            100                 105                 110

aat acc aac ttt gtc atc att cca aat gcc acc cct atg aac tct gcc     384
Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
        115                 120                 125

acc atc agc act atg acc cca gga cag atc aca tac act gct act tct     432
Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
    130                 135                 140

acc aag agt aac acc aaa gaa agc aga gat tct gcc act gcc tcg cca     480
Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
145                 150                 155                 160

cca cca gca cca cct cca cca aac ata ctg cca aca cca tca ctg gag     528
Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
                165                 170                 175

cta gag gaa gca gaa gag cag taa                                    552
Leu Glu Glu Ala Glu Glu Gln
```

180

<210> 38
<211> 183
<212> PRT
<213> Homo sapiens
<400> 38

Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
1 5 10 15

Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
20 25 30

Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
35 40 45

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
50 55 60

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
65 70 75 80

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
85 90 95

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
100 105 110

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
115 120 125

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
130 135 140

Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
145 150 155 160

Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
165 170 175

Leu Glu Glu Ala Glu Glu Gln
180

<210> 39
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(552)
<223> Coding sequence for the human DEFB129 gene
<400> 39

```
atg aag ctc ctt ttt cct atc ttt gcc agc ctc atg cta cag tac cag       48
Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
1               5                   10                  15

gtg aac aca gaa ttt att ggc ttg aga cgc tgt tta atg ggt ttg ggg       96
Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
            20                  25                  30

aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc      144
Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
        35                  40                  45

aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa      192
Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
    50                  55                  60

aac tac cta caa tat gga aca cca aat gta ctt aat gaa gac gtc caa      240
Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
65                  70                  75                  80

gaa atg cta aaa cct gcc aag aat tct agt gct gtg ata caa aga aaa      288
Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
                85                  90                  95

cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct      336
His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
            100                 105                 110

aat acc aac ttt gtc atc att cca aat gcc acc cct atg aac tct gcc      384
Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
        115                 120                 125

acc atc agc act atg acc cca gga cag atc aca tac act gct act tct      432
Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
    130                 135                 140

acc aag agt aac acc aaa gaa agc aga gat tct gcc act gcc tcg cca      480
Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
145                 150                 155                 160

cca cca gca cca cct cca cca aac ata ctg cca aca cca tca ctg gag      528
Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
                165                 170                 175

cta gag gaa gca gaa gag cag taa                                     552
Leu Glu Glu Ala Glu Glu Gln
            180
```

<210> 40
<211> 183
<212> PRT
<213> Homo sapiens
<400> 40

```
Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
```

```
1               5                   10                  15

Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
            20                  25                  30

Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
        35                  40                  45

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
    50                  55                  60

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
65                  70                  75                  80

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
                85                  90                  95

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
            100                 105                 110

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
        115                 120                 125

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
    130                 135                 140

Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
145                 150                 155                 160

Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
                165                 170                 175

Leu Glu Glu Ala Glu Glu Gln
            180
```

<210> 41
<211> 372
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1)..(372)
<223> Coding sequence for the variant human DEFB118 gene
<400> 41

```
atg aaa ctc ctg ctg ctg gct ctt cct atg ctt gtg ctc cta ccc caa       48
Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
1               5                   10                  15

gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg       96
```

```
Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
            20                  25                  30

cac cgc agg aaa caa tgc aaa gat gga gaa gca gtg aaa gat aca tgc      144
His Arg Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
        35                  40                  45

aaa aat ctt cga gct tgc tgc att cca tcc aat gaa gac cac agg cga      192
Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
    50                  55                  60

gtt cct gcg aca tct ccc aca ccc ttg agt gac tca aca cca gga att      240
Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
65                  70                  75                  80

att gat gat att tta aca gta agg ttc acg aca gac tac ttt gaa gta      288
Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
                85                  90                  95

agc agc aag aaa gat atg gtt gaa gag tct gag gcg gga agg gga act      336
Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
            100                 105                 110

gag acc tct ctt cca aat gtt cac cat agc tca tga                      372
Glu Thr Ser Leu Pro Asn Val His His Ser Ser
        115                 120
```

<210> 42
<211> 123
<212> PRT
<213> Homo sapiens
<400> 42

```
Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
1               5                   10                  15

Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
            20                  25                  30

His Arg Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
        35                  40                  45

Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
    50                  55                  60

Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
65                  70                  75                  80

Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
                85                  90                  95

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
            100                 105                 110
```

```
Glu Thr Ser Leu Pro Asn Val His His Ser Ser
        115                 120


<210>  43
<211>  372
<212>  DNA
<213>  Homo sapiens
<220>
<221>  CDS
<222>  (1)..(372)
<223>  Coding sequence of the human DEFB118 gene
<400>  43
atg aaa ctc ctg ctg ctg gct ctt cct atg ctt gtg ctc cta ccc caa       48
Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
1               5                   10                  15

gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg       96
Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
            20                  25                  30

cac tgc agg aaa caa tgc aaa gat gga gaa gca gtg aaa gat aca tgc      144
His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
        35                  40                  45

aaa aat ctt cga gct tgc tgc att cca tcc aat gaa gac cac agg cga      192
Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
    50                  55                  60

gtt cct gcg aca tct ccc aca ccc ttg agt gac tca aca cca gga att      240
Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
65                  70                  75                  80

att gat gat att tta aca gta agg ttc acg aca gac tac ttt gaa gta      288
Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
                85                  90                  95

agc agc aag aaa gat atg gtt gaa gag tct gag gcg gga agg gga act      336
Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
            100                 105                 110

gag acc tct ctt cca aat gtt cac cat agc tca tga                      372
Glu Thr Ser Leu Pro Asn Val His His Ser Ser
        115                 120


<210>  44
<211>  123
<212>  PRT
<213>  Homo sapiens
<400>  44

Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
1               5                   10                  15


Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
            20                  25                  30
```

His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
35 40 45

Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
50 55 60

Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
65 70 75 80

Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
85 90 95

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
100 105 110

Glu Thr Ser Leu Pro Asn Val His His Ser Ser
115 120

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 45
aggttgagta tttgccagac 20

<210> 46
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 46
aggacagggg tgagtgata 19

<210> 47
<211> 246
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1)..(246)
<223> Coding sequence for the variant human DEFB126 gene
<400> 47
atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa 48
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga 96
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
20 25 30

```
att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt      144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
        35                  40                  45

tgg gca atg tgc ggc aaa ggg act gct gtg ttc cag ctg aca gac gtg      192
Trp Ala Met Cys Gly Lys Gly Thr Ala Val Phe Gln Leu Thr Asp Val
    50                  55                  60

cta att atc ctg ttt tct gtg tcc aga caa aga cta caa gaa ttt caa      240
Leu Ile Ile Leu Phe Ser Val Ser Arg Gln Arg Leu Gln Glu Phe Gln
65                  70                  75                  80

cag taa                                                             246
Gln
```

<210> 48
<211> 81
<212> PRT
<213> Homo sapiens
<400> 48

```
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1               5                   10                  15

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
            20                  25                  30

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
        35                  40                  45

Trp Ala Met Cys Gly Lys Gly Thr Ala Val Phe Gln Leu Thr Asp Val
    50                  55                  60

Leu Ile Ile Leu Phe Ser Val Ser Arg Gln Arg Leu Gln Glu Phe Gln
65                  70                  75                  80

Gln
```

<210> 49
<211> 336
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1)..(336)
<223> Coding sequence of the human DEFB126 gene
<400> 49

```
atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa       48
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1               5                   10                  15

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga       96
```

```
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
            20                  25                  30

att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt      144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
        35                  40                  45

tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga      192
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
    50                  55                  60

cgt gct aat tat cct gtt ttc tgt gtc cag aca aag act aca aga att      240
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
65                  70                  75                  80

tca aca gta aca gca aca aca gca aca aca act ttg atg atg act act      288
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
                85                  90                  95

gct tcg atg tct tcg atg gct cct acc ccc gtt tct ccc act ggt tga      336
Ala Ser Met Ser Ser Met Ala Pro Thr Pro Val Ser Pro Thr Gly
            100                 105                 110


<210>  50
<211>  111
<212>  PRT
<213>  Homo sapiens
<400>  50

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1               5                   10                  15


Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
            20                  25                  30


Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
        35                  40                  45


Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
    50                  55                  60


Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
65                  70                  75                  80


Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
                85                  90                  95


Ala Ser Met Ser Ser Met Ala Pro Thr Pro Val Ser Pro Thr Gly
            100                 105                 110


<210>  51
<211>  20
<212>  DNA
```

<213> Artificial Sequence
<220>
<223> PCR primer
<400> 51
aatggtgaga aagatgacag 20

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 52
gttgaatgga gggaaagt 18

<210> 53
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Sequencing primer
<400> 53
gtaggtattt atgattag 18

<210> 54
<211> 334
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1)..(333)
<223> Coding sequence for the variant human DEFB126 gene
<400> 54

```
atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa       48
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1               5                   10                  15

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga       96
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
            20                  25                  30

att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt      144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
        35                  40                  45

tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga      192
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
    50                  55                  60

cgt gct aat tat cct gtt ttc tgt gtc cag aca aag act aca aga att      240
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
65                  70                  75                  80

tca aca gta aca gca aca aca gca aca aca act ttg atg atg act act      288
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
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Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
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Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
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Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
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Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
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